

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: NI, JIAN
GENTZ, REINER L.
RUBEN, STEVEN M.

(ii) TITLE OF INVENTION: T1 RECEPTOR-LIKE LIGAND II

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
(B) STREET: 1100 NEW YORK AVENUE, SUITE 600
(C) CITY: WASHINGTON
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/024,348
(B) FILING DATE: 23-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEFFE, ERIC K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.0390001/EKS/AJK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 55..741

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 55..130

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 133..741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGAGGACA ACAGTACCTG ACGCCTCTT CAGCCCGGGA TCGCCCCAGC AGGG ATG	57
Met	
-26	
GGC GAC AAG ATC TGG CTG CCC TTC CCC GTG CTC CTT CTG GCC GCT CTG	105
Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu	
-25 -20 -15 -10	
CCT CCG GTG CTG CTG CCT GGG GCG GCC GGC TTC ACA CCT TCC CTC GAT	153
Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp	
-5 1 5	
AGC GAC TTC ACC TTT ACC CTT CCC GCC GGC CAG AAG GAG TGC TTC TAC	201
Ser Asp Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr	
10 15 20	
CAG CCC ATG CCC CTG AAG GCC TCG CTG GAG ATC GAG TAC CAA GTT TTA	249
Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu	
25 30 35	
GAT GGA GCA GGA TTA GAT ATT GAT TTC CAT CTT GCC TCT CCA GAA GGC	297
Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly	
40 45 50 55	
AAA ACC TTA GTT TTT GAA CAA AGA AAA TCA GAT GGA GTT CAC ACT GTA	345
Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr Val	
60 65 70	
GAG ACT GAA GTT GGT GAT TAC ATG TTC TGC TTT GAC AAT ACA TTC AGC	393
Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser	
75 80 85	
ACC ATT TCT GAG AAG GTG ATT TTC TTT GAA TTA ATC CTG GAT AAT ATG	441
Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn Met	
90 95 100	
GGA GAA CAG GCA CAA GAA CAA GAA GAT TGG AAG AAA TAT ATT ACT GGC	489
Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly	
105 110 115	
ACA GAT ATA TTG GAT ATG AAA CTG GAA GAC ATC CTG GAA TCC ATC AAC	537
Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn	
120 125 130 135	
AGC ATC AAG TCC AGA CTA AGC AAA AGT GGG CAC ATA CAA ACT CTG CTT	585
Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu Leu	
140 145 150	
AGA GCA TTT GAA GCT CGT GAT CGA AAC ATA CAA GAA AGC AAC TTT GAT	633
Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp	
155 160 165	

AGA GTC AAT TTC TGG TCT ATG GTT AAT TTA GTG GTC ATG GTG GTG GTG	681
Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val	
170 175 180	
TCA GCC ATT CAA GTT TAT ATG CTG AAG AGT CTG TTT GAA GAT AAG AGG	729
Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	
185 190 195	
AAA AGT AGA ACT TAAAACTCCA AACTAGAGTA CGTAACATTG AAAATGAGG	781
Lys Ser Arg Thr	
200	
CATAAAAATG CCATAAACTG TTACAGTCCA GACCATTAAT GGTCTCTCC AAAATATTT	841
GAGATATAAA AGTAGGAAAC AGGTATAATT TTAATGTGAA AATTAAGTCT TCACCTTCTG	901
TGCAAGTAAT CCTGCTGATC CAGTTGACT TAAGTGTGTA ACAGGAATAT TTTGCAGAAT	961
ATAGGTTTAA CTGAATGAAG CCATATTAAT AACTGCATTT TCCTAACCTT GAAAAATTT	1021
GCAAATGTCT TAGGTGATTT AAATAATGA GTATTGGGCC TAATTGCAAC ACCAGTCTGT	1081
TTTTAACAGG TTCTATTACC CAGAACTTTT TTGTAAATGC GGCAGTTACA AATTAACTGT	1141
GGAAAGTTTC AGTTTAAGT TATAAACAC CTGAGAATTA CCTAATGATG GATTGAATAA	1201
ATCTTTAGAC TACAAAAAAA AAAAAAAA AAAAAAAA AAA	1244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-26 -25 -20 -15

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-10 -5 1 5

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
25 30 35

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
40 45 50

Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
55 60 65 70

Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
75 80 85

Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn

90	95	100
Met Gly Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr		
105	110	115
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile		
120	125	130
Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu		
135	140	145
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe		
155	160	165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val		
170	175	180
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys		
185	190	195
Arg Lys Ser Arg Thr		
200		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Met Ala Ala Gly Ala Ala Leu Ala Leu Ala Leu Trp Leu Leu Met			
1	5	10	15
Pro Pro Val Glu Val Gly Gly Ala Gly Pro Pro Pro Pro Ile Gln Asp Gly			
20	25	30	
Glu Phe Thr Phe Leu Leu Pro Ala Gly Arg Lys Gln Cys Phe Tyr Gln			
35	40	45	
Ser Ala Pro Ala Asn Ala Ser Leu Glu Thr Glu Tyr Gln Val Ile Gly			
50	55	60	
Gly Ala Gly Leu Asp Val Asp Phe Thr Leu Glu Ser Pro Gln Gly Val			
65	70	75	80
Leu Leu Val Ser Glu Ser Arg Lys Ala Asp Gly Val His Thr Val Glu			
85	90	95	
Pro Thr Glu Ala Gly Asp Tyr Lys Leu Cys Phe Asp Asn Ser Phe Ser			
100	105	110	
Thr Ile Ser Glu Lys Leu Val Phe Phe Glu Leu Ile Phe Asp Ser Leu			
115	120	125	

Gln Asp Asp Glu Glu Val Glu Gly Trp Ala Glu Ala Val Glu Pro Glu
130 135 140
Glu Met Leu Asp Val Lys Met Glu Asp Ile Lys Glu Ser Ile Glu Thr
145 150 155 160
Met Arg Thr Arg Leu Glu Arg Ser Ile Gln Met Leu Thr Leu Leu Arg
165 170 175
Ala Phe Glu Ala Arg Asp Arg Asn Leu Gln Glu Gly Asn Leu Glu Arg
180 185 190
Val Asn Phe Trp Ser Ala Val Asn Val Ala Val Leu Leu Leu Val Ala
195 200 205
Val Leu Gln Val Cys Thr Leu Lys Arg Phe Phe Gln Asp Lys Arg Pro
210 215 220
Val Pro Thr
225

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCCATGGC CGGCTTCACA CCTTCC

26

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCAAGCTTT CATCTATCAA AGTTGCTTTC

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGGATCCG CCATCATGGG CGACAAGATC TGG

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGTACCT CACAATGTTA CGTACTCTAG

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGTACCT CATCTATCAA AGTTGCTTTC

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAT CTATCAAAGT TGCTTTC

57

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACAGAGGG ACTTTCCGAG AGGA 24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGGCAC GAGCTTCTAC CAGCCCAGTC CCCTNAAGGC CTCGCTGGAG ATCGAGTACC	60
AAGTTTTAGA TGGAGCAGGA TTAGATATTG ATTTCCCATC TTGCCTCTCC AGAAGGCAAA	120
ACCTTAGTTT TTGAACAAAG AAAATCAGAT GGAGTTCACCA CGTGTATAAG AAGTAAAAAT	180
GGGCCAGGCA CTGCGGTTCA CGCCTATAAT CCCAGCACTT TCCGAGGCCG AGTGTAGAGA	240
CTGAAGTTGG TGATTACATG TTCTGCTTTG ACAATACATT CAGCACCATT TCTGAGAAGG	300
TGATTTCTT TGAATTAATC CTGGATAATA TGGGAGGACA GGCACAAGAC AAGAGGTTG	360
GAGNATATT ACTGGCCNAT TTATGGTATG	390

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGACTCCAGA TTTCCCTGTC AACACGAGG AGTCCAGAGA GGAAACGCGG AGANGAACAA	60
CAGTACCTGA CGCCTCTTTC AGCCCGGGAT CGCCCCAGCA GGGATGGGCG ACAAGATCTG	120

GCTGCCCTTC	CCCGTGCTCC	TTCTGGCCGC	TCTGCCTCCG	GTGCTGCTGC	CTNGGGNCGG	180
CCGGCTTCAC	ACCTTCCCTC	GATAGCGACT	TCACCTTTAC	CCTTCCCGCC	GGCCAGAAGG	240
AGTGCTTCTA	CCAGCCCCATG	CCCCTGAAGG	CCTCGCTGGA	GATCGAGTAC	CAAGTTTTAG	300
ATGGAGCAGG	ATTAGATATT	GATTTCCATC	TTGCCTCTCC	AGAAGGCAAA	ACCTTAGTTT	360
TTGAACAAAG	AAAATCAGAT	GGAGTTCACA	CTGTAGAGAC	TGAAGTTGGT	GATTACATGT	420
TCTGCTTGA	CAATACATTC	AGCACCATT	CTGAGAAGGT	GATTTCTTT	GAATTAATCC	480
TGGATAATAT	GGGAGAACAG	GCACAAGAAC	AAGAAGATTG	GAAGAAATAT		530

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGACTCCAGA	TTTCCCTGTC	AACCACGAGG	AGTCCAGAGA	GGAAACGCGG	AGCGCACAAC	60
AGTACCTGAC	GCCTCTTCA	GCCCAGGATC	GCCCCAGCAG	GGATGGGCGA	CAAGATCTGG	120
CTGCCCTTCC	CCGTGCTCCT	TCTGGCCGCT	CTGCCTCCGG	TGCTGCTGCC	TGGGGCGGCC	180
GGCTTCACAC	CTTCCCTCGA	TAGCGACTTC	ACCTTTACCC	TTCCCGCCGG	CCAGAAGGAG	240
TGCTTCTACC	AGCCCAGGCC	CCTGAAGGCC	TCGCTGGAGA	TCGAGTACCA	AGTTTTAGAT	300
GGAGCAGGAT	TAGATATTGA	TTTCCATCTT	GCCTCTCCAG	AAGGCAAAAC	CTTAGTTTT	360
GAACAAAGAA	AATCAGATGG	AGTCACACT	GTAGAGACTG	AAGTTGGTGA	TTACATGTT	420
TGCTTGACA	ATACATTCA	CACCATTCT	GAGAAGGTGA	TTT		463

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCAGAAATATA	GGTTAACTG	AATGAAGCCA	TATTAATAAC	TGCATTTGCC	TAACTTGGAA	60
-------------	-----------	------------	------------	------------	------------	----

AAGTTGGCA AATGTCTTAG GTGATTTAAA TAAATGAGTA TTGGGCCTAA TTGCCACACC	120
AGTCTGTTT GAACAGGTTTC TATTACCCAG AACCTTTTG TAAATGCGGC AGTTACAAAT	180
TAACGTGG AGGTTT	196

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCAAAACCTT AGTTTGAA CAAAGAAAAT CAGATGGAGT TCACACTGTA GAGACTGAAG	60
TTGGTGATTA CATGTTCTGC TTTGACAATA CATTCAAGCAC CATTCTGAG AAGGTGATT	120
TCTTGAAATT AATCCTGGAT AATATGGGAG AACAGGCACA AGAACAAAGAA GATTGGAAGA	180
AATATATTAC TGGCACAGAT ATATTGGATA TGAAAATGGA AGACATCCTG GAATCCATCA	240
ACAGCATCAA GTCCAGACTA AGCAAAAGTG GGCACATACA AACTCTGCTT AGAGCATTG	300
AAGCTCGTGA TCGAACATA CAAGAAAGCA ACTTTGATAG AGTCAATTTC TGGTCTATGG	360
TTAATTAGT GGTCATGGTG GTGGTGTAG CCATTCAAGT TTATATGCTG AAGAGTCTGG	420
TTTGAAGATN AGGAGGGAAA GTTGGAACTT AAAACTCCCA AACTTGGTA CGGNACCTTG	480
NAAAATGGGG CCATTAAC TGCCATTAAAC NGGTTCCAGC	520

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGACTCCAGA TTTCCCTGTC AACCACGAGG AGTCCAGAGA GGAAACGCGG AGATGAACAA	60
CAGTACCTGA CGCCTCTTTC AGCCCGGGAT CGCCCCAGCA GGGATGGCG ACAAGATCTG	120
GCTGCCCTTC CCCGTGCTCC TTCTGGCCGC TCTGCCTCCG GTGCTGCTGC CTGGGNGGCC	180
GGCTTCACAC CTTCCCTCGA TAGCGACTTC ACCTTTACCC TTCCCGCCGG CCAGAAGGAG	240

TGCTTCTACC AGCCCATGCC CCTGAAGGCC TCGCTGGAGA TCGAGTACCA AGTTTTAGAT	300
GGAGCAGGAT TAGATATTGA TTTCCATCTT GCCTCTCCAG AAGGCAAAAC CTTAGTTTT	360
GAACAAAGAA AATCAGATGG GAGTCACAC TGTAAGAGAC TGAAGTTGGG TGATTACATG	420
TTCTGCTTG ACAATACATT CAGCACCATT TCTGAGAAGG TGATTCTTT GGAATTA	477

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTCTAAA GATTATTCA ATCCATCATT AGGTAAATTCT CAGGTGATT ATAACCTAAA	60
ACTGAAAACT TCCACAGTTA ATTTGTAACT GCCGCATTTA CAAAAAAAGTT CTGGGTAATA	120
GAACCTGTTA AAAACAGACT GGTGTTGCAA TTAGGCCAA TACTCATTAA TTTAAATCAC	180
CTAAGACATT TGCAAAATT TTCAAAGTTA GGAAAATGCA GTTATTAATA TGGCTTCATT	240
CAGTTAAACC TATATTCTGC AAAATATTCC TGTTACACAC TTAAGGTACA ACTGGATCAG	300
CAGGATTACT TGCACAGAAA GNTGAAGACT TAATTTCAC ATTAAAATTA TACCTGGTT	360
CCTACTTTA TATCNCAAAA TATTTGGGA GAAGACCATT AAT	403

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACCTGACGC CTCTTCAGC CCGGGATCGC CCCAGCAGGA ATGGGCGACA AGATCTGGCT	60
GCCCTTCCCG TGCTCCTTCT GGCGCCTCTG CTCCGGTGCT GCTGCCTGGG NGGCCGGCTT	120
CACACCTTCC CTCGATAGCG ACTTCACCTT TACCTTCCGC CGGCAGAAGG AGTGCCTNCTA	180
CCAGCCATGC NCCTGAAGGC CTCNCTGGAG ATCGAGTACC AAGTTTTAGA TGGAGCAGGA	240
TTAGATATTG ATTTCCATCT TGCCTCTCCA AGAAAGGCAA AACCTTAAGT TTTTGAACAA	300

AGAAATCAGA TGGAGTCAC ACTGTAGAGA CTGAAAGTTG GTGATTACAT GTTCTGCTT	360
GACAATACAT TCAAGAACCA TTTCTGAGAA GGTGAT	396

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGAAGGAG TGCTTCTACC AGCCCATGCC CCGTGAAGGC CTCGCTGGAG ATCGAGTACC	60
AAGTTTTAGA TGGAGCAGGA TTAGATATTG ATTTCCATCT TGCCTCTCCA GAAGGCAAAA	120
CCTTAGTTTT TGAACAAAGA AAATCAGATG GAGTCACAC TGTAGAGACT GAAGTTGGTG	180
ATTACATGTT CTGCTTGAC AATACATTCA GCACCATTTC TGAGAAGGTG ATTTTCTTTG	240
ATTAATCCT GGATAATATG GGAGAACAAAG GCACAAGAAC AAGAAGATTG GAAGAAATAT	300
ATTACTGGC	309

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATTGATTCC ATCTGCCTC TCCAGAAGGC AAAACCTTAG TTTTGAAACA AAGAAAATCA	60
GATGGAGTTC ACACTGTAGA GACTGAAGTT GGTGATTACA TGTCTGCTT TGACAATACA	120
TTCAGCACCA TTTCTGAGAA GGTGATTTTC TTTGAATTAA TCCTGGATAA TATGGGAGAA	180
CAGGCACAAG AACAAAGAAGA TTGGAAGAAA TATATTACTG GCACAGATAT ATTGGATATG	240
AAACTGGAAG ACATCCTGGG AATCCATCAA CAGCATCAAG TCCAGACTAA GGCAAAAGTG	300
GGGCACATAC AAACCTCTGCT TAGGAGCATT TGGAAAGGCTC GTGGATCCGA AACATTACAA	360
GGAAAGGCAA CTTTGGATTA GGAGTCCAAT TTCTGGGTCT ATGGGTTAAT TTAGTGGGTC	420
ATGGTGGTGG TGTCAGCCT TCAGTTATA TGGCTGGAGG NT	462

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGCGGAGAN GGACAAACAGT ACCTGACGCC TCTTCAGCC CGGGATCGCC CCACCAGGGA	60
ATGGGCGACA AGATCTGGCT GCCCTTCCCC GTGCTCCTTC TGGCCGCTCT GCCTCCGGTG	120
CTGCTGCCTG GGGGGCCGGC TTCACACCTT CCCTCGATAG CGACTTCACC TTTACCCTTC	180
CCGCCGGCCA GAAGGAGTGC TTCTACCAGC CCATGCCCT GAAGGCCTCG CTGGGAGATC	240
GAGTACCAAG TTTAGATGG AGCAGGATTA GATATTGATT TCCATCTTGC CTCTCCAGAA	300
GGGCAAAACC TTAGTTTTG GAACAAAGGA AAATCAGGTG GGAGTTTCAC ANTGTAGGAG	360
GATTGAAGTT GGGTGGATT ACATGTTCT GGTTTTGAC AATTACATTT CAGGCACCNT	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCGGAGACG NATCAACAGT ACCTGACGCC TCTTCAGCC CGGGATCGCC CCAGCAGGAT	60
TGGGCGACAA GATCTGGCTG CCCTTCCCCG TGCTCCTTCT GGCCGCTCTG CCTCCGGTGC	120
TGCTGCCTGG GGGGCCGGCT TCACACCTTC CCTCGATAGC GACTTCACCT TTACCCCTCC	180
CGCCGGCCAG AAGGAGTGC TCTACCAGCC CATGCCCTG AAGGCCTCGC TGGGAGATCG	240
AGTACCAAGT TTTAGATGGG AGCAGGATTA GATATTGATT TTCCATCTTGC CCTCTCCAGA	300
AGGGCAAAAC CTTAGTTTT TGAACAAAGG AAAATCAGGT GGGGAGTTTC ACAATGTAGG	360
AGGATTGAAG TTTGGGTGAT TTACATGTT TTGCTTTGA ACAATTACAT TTCAGGCANC	420
ATTTTTGAGG NAGGGTGAAT TTTCTTGGA	450

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAATAACTGC ATTTCTCAA CTTTGAAAAA TTTGCAAAT GTCTAGGTG ATTTAAATAA	60
ATGAGTATTG GGCTTAATTG CAACACCAAGT CTGTTTTAA CAGGTTCTAT TACCCAGAAC	120
TTTTTGTAATGCGGCAGT TACAAATTAA CTGTGGAAGT TTTCAGTTT AAGTTATAAA	180
TCACCTGAGA ATTACCTAAT GATGGATTGA ATAAATCTTT AGACTACAAA AGCCCAACTT	240
TTCTCTATTT ACATATGCAT CTCTCCTATA ATGTAAATAG AATAATAGCT TTGAAATACA	300
ATTAGGTTT TGAGATTTT ATAACCAAAT ACATTCAGT GTAACATATT AGCAGAAAGC	360
ATTAGTCCTT GGACTTTGCT TACATTCCA AAAGCTGACA TT	402

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCCATCTTG CCTCTCCAGA AGGCAAAACC TTGTTTTG AACAAAGAAA ATCAGATGGA	60
GTTCACACTG TAGAGACTGA AGTTGGTGAT TACATGTTCT GCTTGACAA TACATTCA	120
ACCATTCTG AGAAGGTGAT TTTCTTGAA TTAATCCTGG ATAATATGGG AGAACAGGCA	180
CAGGAACAAG AGGATTGGGA GGAATATATT ACTGGCACAG ATATATTGGA TATGAAC	240
AGACATCTGG ATCATCACAG CATCAGTCCA GACTAGCAA GTGGGCACAT CAACTCTCTT	300
AGGCATTTG	309

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGACTCCAGA TTTCCCTGTC AACCACGAGG AGTCCAGAGA GAAAACGCGG AGATGAGCAA	60
GCAGTACCTG ACGCCTCTTT CAGCCCAGGA TCGCCCCAGC AGGGATGGGC GACAAGATCT	120
GGCTGCCCTT CCCC GTGCTC CTTCTGGCCG CTCTGCCTCC GGTGCTGCTG CCTGGGCAGC	180
CGGCTTCACA CCTTCCCTCG ATAGCGACTT CACCTTTACC CTTCCCGCCG GCCAGAAGGA	240
GTGCTTCTAC CAGCCCATGC GCCTGAAAGC CTCTCTTGAG ATCGAG	286

SKGF_DC1:56409.1

\